



## SEQUENCE LISTING

<110> Cohen, Daniel  
Blumenfeld, Marta  
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Bougueleret, Lydie

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<141> 2001-07-09

<150> 08/996,306  
<151> 1997-12-22

<150> 60/099,658  
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<150> 09/218,207  
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<150> 09/338,907  
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gttctgcaat	tttataaatg	ttcatgtctt	tttttaaaaa	aggtgctatc	gaaattctgt	5072
gtctccagca	ggcaagaata	cttgactaac	tctttttgtc	tctttatggg	atcttcagaa	5132
taaagtctga	cttgtgtttt	tgagattatt	ggtgcctcat	taattcagca	ataaaggaaa	5192
atatgcattt	caaaaanaaa	aaaaaaaaaa	aaaaa			5227

&lt;210&gt; 4

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; HELIX

&lt;222&gt; 1..33

&lt;223&gt; Rao and Argos identification method, potential helix

&lt;221&gt; HELIX

&lt;222&gt; 4..20

&lt;223&gt; Klein, Kanehisa and DeLisi identification method, potential helix

&lt;221&gt; HELIX

&lt;222&gt; 4..24

&lt;223&gt; Eisenberg, Schwarz, Komarony, Wall identification method, potential helix

<221> HELIX  
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<223> Eisenberg, Schwarz, Komarony, Wall identification method,  
potential helix

<221> CARBOHYD  
<222> 57..59  
<223> Prosite match

<221> HELIX  
<222> 76..96  
<223> Eisenberg, Schwarz, Komarony, Wall identification method,  
potential helix

<221> PHOSPHORYLATION  
<222> 78  
<223> potential Tyrosine kinase site, Prosite match

<221> PHOSPHORYLATION  
<222> 84  
<223> potential caseine kinase II site, Prosite match

<221> SITE  
<222> 94..115  
<223> potential Leucine zipper site, Prosite match

<221> MYRISTATE  
<222> 119..123  
<223> potential site, Prosite match

<221> PHOSPHORYLATION  
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<223> potential protein kinase C, Prosite match

<221> PHOSPHORYLATION  
<222> 147  
<223> potential caseine kinase II site, Prosite match

<221> PHOSPHORYLATION  
<222> 194  
<223> potential protein kinase C, Prosite match

<221> PHOSPHORYLATION  
<222> 215  
<223> potential Tyrosine kinase site, Prosite match

<221> SULFATATION  
<222> 221  
<223> Prosite match

<221> PHOSPHORYLATION  
<222> 233  
<223> potential cAMP and cGMP dependant protein kinase site, Prosite

<223> potential caseine kinase II site, Prosite match

<221> PHOSPHORYLATION

<222> 306

<223> potential protein kinase C, Prosite match

<221> HELIX

<222> 310..330

<223> Eisenberg, Schwarz, Komarony, Wall identification method,  
potential helix

<221> MYRISTATE

<222> 319..323

<223> Prosite match

<221> MYRISTATE

<222> 323..327

<223> Prosite match

<221> AMIDATION

<222> 329

<223> Prosite match

<221> HELIX

<222> 333..353

<223> Eisenberg, Schwarz, Komarony, Wall identification method,  
potential helix

<221> MYRISTATE

<222> 341..345

<223> Prosite match

<221> PHOSPHORYLATION

<222> 350

<223> potential protein kinase C, Prosite match

<400> 4

Met	Arg	Tyr	Leu	Leu	Pro	Ser	Val	Val	Leu	Leu	Gly	Thr	Ala	Pro	Thr
1			5						10					15	
Tyr	Val	Leu	Ala	Trp	Gly	Val	Trp	Arg	Leu	Leu	Ser	Ala	Phe	Leu	Pro
		20					25					30			
Ala	Arg	Phe	Tyr	Gln	Ala	Leu	Asp	Asp	Arg	Leu	Tyr	Cys	Val	Tyr	Gln
	35					40					45				
Ser	Met	Val	Leu	Phe	Phe	Phe	Glu	Asn	Tyr	Thr	Gly	Val	Gln	Ile	Leu
	50				55					60					
Leu	Tyr	Gly	Asp	Leu	Pro	Lys	Asn	Lys	Glu	Asn	Ile	Ile	Tyr	Leu	Ala
65				70					75					80	
Asn	His	Gln	Ser	Thr	Val	Asp	Trp	Ile	Val	Ala	Asp	Ile	Leu	Ala	Ile
		85					90						95		
Arg	Gln	Asn	Ala	Leu	Gly	His	Val	Arg	Tyr	Val	Leu	Lys	Glu	Gly	Leu
	100						105				110				
Lys	Trp	Leu	Pro	Leu	Tyr	Gly	Cys	Tyr	Phe	Ala	Gln	His	Gly	Gly	Ile
	115					120					125				
Tyr	Val	Lys	Arg	Ser	Ala	Lys	Phe	Asn	Glu	Lys	Glu	Met	Arg	Asn	Lys

165 170 175  
 Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val Leu Lys His Val  
 180 185 190  
 Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys Met Lys  
 195 200 205  
 Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu Gly Lys  
 210 215 220  
 Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met Thr Glu Phe Leu  
 225 230 235 240  
 Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp Arg Ile Asp Lys  
 245 250 255  
 Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu His Glu  
 260 265 270  
 Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro  
 275 280 285  
 Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys  
 290 295 300  
 Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu  
 305 310 315 320  
 Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn  
 325 330 335  
 Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys  
 340 345 350  
 Ala

&lt;210&gt; 5

&lt;211&gt; 364

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

Met Leu Leu Ser Leu Val Leu His Thr Tyr Ser Met Arg Tyr Leu Leu  
 1 5 10 15  
 Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp  
 20 25 30  
 Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln  
 35 40 45  
 Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe  
 50 55 60  
 Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu  
 65 70 75 80  
 Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala Asn His Gln Ser Thr  
 85 90 95  
 Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu  
 100 105 110  
 Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu  
 115 120 125  
 Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser  
 130 135 140  
 Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val  
 145 150 155 160  
 Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg  
 165 170 175  
 Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala

210	215	220
Ile Tyr Asp Val Thr Val Val Tyr Glu Gly Lys Asp Asp Gly Gly Gln		
225	230	235
Arg Arg Glu Ser Pro Thr Met Thr Glu Phe Leu Cys Lys Glu Cys Pro		240
	245	250
Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro Glu		255
	260	265
Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys		270
	275	280
Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg Arg		285
	290	295
Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys		300
305	310	315
Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu		320
	325	330
Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr Gly		335
	340	345
Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala		350
	355	360

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 <212> DNA  
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 ctgtccctgg tgctccacac gtactc

26

<210> 7  
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 <223> primer oligonucleotide GC1.5p.2

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26

<210> 8  
 <211> 27  
 <212> DNA  
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<400> 8  
caatatctgg accccggtgt aattctc 27

<210> 9  
<211> 34  
<212> DNA  
<213> Homo Sapiens

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<221> misc\_feature  
<222> 1..34  
<223> primer oligonucleotide GC1.3p

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cttgctgtct ggagacacag aatttcgata gcac 34

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<212> DNA  
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<223> primer oligonucleotide PGRT32

<400> 10  
tttttttttt tttttttttg aaat 24

<210> 11  
<211> 6  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> 160..165  
<223> box2 from SEQID4, present in AF003136, P33333, P26647, U89336,  
U56417, AB005623.

<400> 11  
Phe Pro Glu Gly Thr Arg  
1 5

<210> 12  
<211> 6  
<212> PRT  
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<400> 12  
Phe Pro Glu Gly Thr Asp  
1 5

<210> 13  
<211> 6  
<212> PPT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> 223..228  
<223> box2 from P38226, Z49770

<400> 13  
Phe Pro Glu Gly Thr Asn  
1 5

<210> 14  
<211> 6  
<212> PPT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> 90..95  
<223> box2 from Z49860 and Z29518

<400> 14  
Phe Val Glu Gly Thr Arg  
1 5

<210> 15  
<211> 9  
<212> PPT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> 211..219  
<223> box3 from SEQID4, present in AF003136

<400> 15  
Leu Asp Ala Ile Tyr Asp Val Thr Val  
1 5

<210> 16  
<211> 9  
<212> PPT

<222> 204..212

<223> box3 from Z72511

<400> 16

Val Glu Tyr Ile Tyr Asp Ile Thr Ile

1 5

<210> 17

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> 271..279

<223> box3 from P38226

<400> 17

Ile Glu Ser Leu Tyr Asp Ile Thr Ile

1 5

<210> 18

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> 265..273

<223> box3 from Z49770

<400> 18

Leu Asp Ala Ile Tyr Asp Val Thr Ile

1 5

<210> 19

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> 138..146

<223> box3 from Z49860

<400> 19

Val Pro Ala Ile Tyr Asp Met Thr Val

1 5

<210> 20

<220>  
 <221> SITE  
 <222> 218..226  
 <223> box3 from Z29518

<400> 20  
 Val Pro Ala Ile Tyr Asp Thr Thr Val  
 1 5

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 <222> 24  
 <223> polymorphic base C

<221> primer\_bind  
 <222> 1..23  
 <223> potential microsequencing oligo 99-123.mis1

<221> primer\_bind  
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 <223> complement potential microsequencing oligo 99-123.mis2

<400> 21  
 tttctcatcc tcacacctca ctgcgcccct cctgaacca ctccctt

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<210> 22  
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 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 1..47  
 <223> polymorphic fragment 4-26

<221> allele  
 <222> 24  
 <223> polymorphic base G

<221> primer\_bind  
 <222> 1..23  
 <223> potential microsequencing oligo 4-26.mis1

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ccctgtnaga cagctcctgt atcgttgttg agatgggaaa gtgcatac

47

<210> 23  
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<221> primer\_bind  
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<223> potential microsequencing oligo 4-14.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 4-14.mis2

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gcagggagca gaccagacat gattgttct agtctagctg attcata

47

<210> 24  
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<212> DNA  
<213> Homo Sapiens

<220>  
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<223> polymorphic fragment 4-77, extracted from SEQ ID1 12057 12103

<221> allele  
<222> 24  
<223> polymorphic base C

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 4-77.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 4-77.mis2

<400> 24  
gctgttcaga ctaaacttgg agactacagt cagtcagaga acttgct

47

<212> DNA  
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<220>  
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<222> 1..47  
<223> polymorphic fragment 99-217, extracted from SEQ ID1 34469 34515

<221> allele  
<222> 24  
<223> polymorphic base C

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-217.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-217.mis2

<400> 25  
atatagttca cgttatgttc atacttaatt gttgcatttt gtttgcc

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<210> 26  
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<220>  
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<223> polymorphic fragment 4-67, extracted from SEQ ID1 51612 51658

<221> allele  
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<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 4-67.mis1

<221> primer\_bind  
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<400> 26  
gccagtga aa tacagactta attcgatg actgaacgaa tttgttt

47

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<223> polymorphic fragment 99-213

<221> allele

<222> 24

<223> polymorphic base T

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 99-213.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-213.mis2

<400> 27

ccttagcatt caagcccctg agctctggtg ttgtccaccc ctggggg

47

<210> 28

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<212> DNA

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<223> polymorphic fragment 99-221

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<223> polymorphic base A

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 99-221.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-221.mis2

<400> 28

agcttgagaa accagaaaag ccaaaaaggag gctcctacca catgggt

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<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-135.mis2

<400> 29  
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<223> base T ; C in SEQ ID21

<221> primer\_bind  
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<223> potential microsequencing oligo 99-123.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-123.mis2

<400> 30  
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<210> 31  
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<222> 1..47  
<223> polymorphic fragment 4-26, variant version of SEQ ID22

<221> allele  
<222> 24  
<223> base A ; G in SEQ ID22

<221> primer\_bind  
<222> 1..23

<223> complement potential microsequencing oligo 4-26.mis2

<400> 31

ccctgttnaga cacgtcctgt atcattgttg agatgggaaa gtgcatc

47

<210> 32

<211> 47

<212> DNA

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<221> allele

<222> 1..47

<223> polymorphic fragment 4-14, variant version of SEQ ID23

<221> allele

<222> 24

<223> base C ; T in SEQ ID23

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 4-14.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-14.mis2

<400> 32

gcagggagca gaccagacat gatctgttct agtctagctg attcata

47

<210> 33

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<221> allele

<222> 1..47

<223> polymorphic fragment 4-77, variant version of SEQ ID24

<221> allele

<222> 24

<223> base G ; C in SEQ ID24

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 4-77.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-77.mis2

<210> 34  
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<223> polymorphic fragment 99-217, variant version of SEQ ID25

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<223> base T ; C in SEQ ID25

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<221> allele  
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<223> base T ; C in SEQ ID26

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<222> 1..23  
<223> potential microsequencing oligo 4-67.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 4-67.mis2

<400> 35  
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47

<210> 36  
<211> 47

<221> allele  
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<223> polymorphic fragment 99-213, variant version of SEQ ID27

<221> allele  
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<223> base C ; T in SEQ ID27

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-213.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-213.mis2

<400> 36  
ccttagcatt caagcccttg agccctggtg ttgtccaccc ctggggg

47

<210> 37  
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<223> polymorphic fragment 99-221, variant version of SEQ ID28

<221> allele  
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<223> base C ; A in SEQ ID28

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-221.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-221.mis2

<400> 37  
agcttgagaa accagaaaag ccacaaggag gctcctacca catgggt

47

<210> 38  
<211> 47  
<212> DNA  
<213> Homo Sapiens

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<223> base G ; A in SEQ ID29

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 99-135.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-135.mis2

<400> 38

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47

<210> 39

<211> 18

<212> DNA

<213> Homo Sapiens

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<223> upstream amplification primer 99-123-PU

<400> 39

aaagccagga ctagaagg

18

<210> 40

<211> 18

<212> DNA

<213> Homo Sapiens

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<221> misc\_feature

<222> 1..18

<223> upstream amplification primer 4-26-PU

<400> 40

tacagccctg taagacac

18

<210> 41

<211> 18

<212> DNA

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<220>

<221> misc\_feature

<222> 1..18

<223> upstream amplification primer 4-14-PU

<400> 41

tctaagctct catccaac

18

<212> DNA  
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11947

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tggtgattta caggcggc 18

<210> 43  
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<222> 1..19  
<223> upstream amplification primer 99-217-PU, extracted from SEQ ID1 34216  
34234

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ggtgggaatt tactatatg 19

<210> 44  
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<221> misc\_feature  
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<223> upstream amplification primer 4-67-PU, extracted from SEQ ID1 51596  
51613

<400> 44  
aagttcacct tctcaagc 18

<210> 45  
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<221> misc\_feature  
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<400> 45

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<212> DNA  
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<223> upstream amplification primer 99-221-PU

<400> 46  
ccctttttct tcactgttc 19

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<223> upstream amplification primer 99-135-PU

<400> 47  
tggaagttgt tattgccc 18

<210> 48  
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tattcagaaa ggagtggg 18

<210> 49  
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tgaggactgc taggaaag 18

<213> Homo Sapiens

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<213> Homo Sapiens

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<221> misc\_feature

<222> 1..20

<223> downstream amplification primer 4-77-RP, extracted from SEQ ID1 12339  
123

58 complement

<400> 51

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20

<210> 52

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<223> downstream amplification primer 99-217-RP, extracted from SEQ ID1 34625  
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<400> 52

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21

<210> 53

<211> 20

<212> DNA

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520

15 complement

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<223> downstream amplification primer 99-135-RP

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<210> 57  
<211> 47  
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<221> allele  
<222> 24

<223> potential microsequencing oligo 99-1482.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1482.mis2

<400> 57

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47

<210> 58

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-73, extracted from SED ID1 13657 13703

<221> allele

<222> 24

<223> polymorphic base C in PG1 (13680) SEQ ID1

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 4-73.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-73.mis2

<400> 58

gttttcctta tgatgttaca tggcttattt ttaaaggtaa tgaaaac

47

<210> 59

<211> 47

<212> DNA

<213> Homo Sapiens

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<221> allele

<222> 1..47

<223> polymorphic fragment 4-65, extracted from SEQ ID1 51448 51494

<221> allele

<222> 24

<223> polymorphic base T in PG1 (51471) SEQ ID1

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 4-65.mis1

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47

<210> 60  
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<220>  
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<223> polymorphic fragment 99-1482, variant version of SEQ ID57

<221> allele  
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<223> base A ; C in SEQ ID57

<221> primer\_bind  
<222> 1..23  
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47

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<222> 1..47  
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<221> primer\_bind  
<222> 1..23  
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<221> primer\_bind  
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47

<212> DNA  
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<221> allele  
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<221> primer\_bind  
<222> 1..23  
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<221> primer\_bind  
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4 /

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21

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13564

<400> 64  
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18

<210> 65

<220>  
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51168

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<400> 66  
acaaatctat ataaggctgg 20

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13981 complement

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<210> 68  
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<212> DNA  
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51499 complement

<400> 68  
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&lt;400&gt; 69

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Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
    10           15           20

cgg ctg ctc tcc gcc ttc ctg ccc gcc cgc ttc tac caa gcg ctg gac      150
Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
    25           30           35           40

gac cgg ctc tac tgc gtc tac cag agc atg gtg ctc ttc ttc ttc gag      198
Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
           45           50           55

aat tac acc ggg gtc cag ata ttg cta tat gga gat ttg cca aaa aat      246
Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu Pro Lys Asn
           60           65           70

aaa gaa aat ata ata tat tta gca aat cat caa agc aca gtt gac tgg      294
Lys Glu Asn Ile Ile Tyr Leu Ala Asn His Gln Ser Thr Val Asp Trp
           75           80           85

att gtt gct gac atc ttg gcc atc agg cag aat gcg cta gga cat gtg      342
Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu Gly His Val
           90           95           100

cgc tac gtg ctg aaa gaa ggg tta aaa tgg ctg cca ttg tat ggg tgt      390
Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu Tyr Gly Cys
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tac ttt gct cag cat gga gga atc tat gta aag cgc agt gcc aaa ttt      438
Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe
           125           130           135

aac gag aaa gag atg cga aac aag ttg cag agc tac gtg gac gca gga      486
Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly
           140           145           150

act cca atg tat ctt gtg att ttt cca gaa ggt aca agg tat aat cca      534
Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro
           155           160           165

gag caa aca aaa gtc ctt tca gct agt cag gca ttt gct gcc caa cgt      582
Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg
           170           175           180

ggc ctt gca gta tta aaa cat gtg cta aca cca cga ata aag gca act      630
Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg Ile Lys Ala Thr
    185           190           195           200

cac gtt gct ttt gat tgc atg aag aat tat tta gat gca att tat gat      678
His Val Ala Phe Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp
           205           210           215

gtt acg gtg gtt tat gaa ggg aaa gac gat gga ggg tag cgaagagagt      727
Val Thr Val Val Tyr Glu Gly Lys Asp Asp Gly Gly *
           220           225

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gtatcgacaa aaaagatgtc ccagaagaac aagaacatat gagaagatgg ctgcatgaac      847
gtttcgaaat caaagataag atgcttatag aattttatga gtcaccagat ccagaaagaa      907
gaaaaagatt tcttgggaaa agtggttaatt ccaaattaag tatcaagaag actttaccat      967
caatgttgat cttaagtggg ttgactgcag gcatgcttat gaccgatgct ggaaggaagc      1027
tgtatgtgaa cacctggata tatggaaccc tacttggtctg cctgtggggtt actattaaag      1087
cataqacaaq tagctgtctc cagacagtgg gatgtgctac attgtctatt tttggcggct      1147

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at tt t t g c a a g	t c a g a t g g c t	g c a t t t t t t g a	g c a t t a a t t t t	g c a g c g t a t t	t c a c t t t t t t c	1447
t g t t a t t t t c	a a t t t a t t a c	a a c t t g a c a g	c t c c a a g c t c	t t a t t a c t a a	a g t a t t t a g t	1507
a t c t t g c a g c	t a g t t a a t a t	t t c a t c t t t t	g c t t a t t t t c t	a c a a g t c a g t	g a a a t a a a t t	1567
g t a t t t a g g a	a g t g t c a g g a	t g t t c a a a g g	a a a g g g t a a a	a a g t g t t c a t	g g g g a a a a a g	1627
c t c t g t t t a g	c a c a t g a t t t	t a t t g t a t t g	c g t t a t t a g c	t g a t t t t a c t	c a t t t t a t a t	1687
t t g c a a a a t a	a a t t t t c t a a t	a t t t a t t g a a	a t t g c t t a a t	t t g c a c a c c c	t g t a c a c a c a	1747
g a a a a t g g t a	t a a a a t a t g a	g a a c g a a g t t	t a a a a t t g t g	a c t c t g a t t c	a t t a t a g c a g	1807
a a c t t t a a a t	t t c c c a g c t t	t t t g a a g a t t	t a a g c t a c g c	t a t t a g t a c t	t c c c t t t g t c	1867
t g t g c c a t a a	g t g c t t g a a a	a c g t t a a g g t	t t t c t g t t t t	g t t t t g t t t t	t t t a a t a t c a	1927
a a a g a g t c g g	t g t g a a c c t t	g g t t g g a c c c	c a a g t t c a c a	a g a t t t t t a a	g g t g a t g a g a	1987
g c c t g c a g a c	a t t c t g c c t a	g a t t t a c t a g	c g t g t g c c t t	t t g c c t g c t t	c t c t t t g a t t	2047
t c a c a g a a t a	t t c a t t c a g a	a g t c g c g t t t	c t g t a g t g t g	g t g g a t t c c c	a c t g g g c t c t	2107
g g t c c t t c c c	t t g g a t c c c g	t c a g t g g t g c	t g c t c a g c g g	c t t g c a c g t a	g a c t t g c t a g	2167
g a a g a a a t g c	a g a g c c a g c c	t g t g c t g c c c	a c t t t c a g a g	t t g a a c t c t t	t a a g c c c t t g	2227
t g a g t g g g c t	t c a c c a g c t a	c t g c a g a g g c	a t t t t g c a t t	t g t c t g t g t c	a a g a a g t t c a	2287
c c t t c t c a a g	c c a g t g a a a t	a c a g a c t t a a	t t c g t c a t g a	c t g a a c g a a t	t t g t t t a t t t	2347
c c c a t t a g g t	t t a g t g g a g c	t a c a c a t t a a	t a t g t a t c g c	c t t a g a g c a a	g a g c t g t g t t	2407
c c a g g a a c c a	g a t c a c g a t t	t t t a g c c a t g	g a a c a a t a t a	t c c c a t g g g a	g a a g a c c t t t	2467
c a g t g t g a a c	t g t t c t a t t t	t t g t g t t a t a	a t t t a a a c t t	c g a t t t c c t c	a t a g t c c t t t	2527
a a g t t g a c a t	t t c t g c t t a c	t g c t a c t g g a	t t t t t g c t g c	a g a a a t a t a t	c a g t g g c c c a	2587
c a t t a a a c a t	a c c a g t t g g a	t c a t g a t a a g	c a a a a t g a a a	g a a a t a a t g a	t t a a g g g a a a	2647
a t t a a g t g a c	t g t g t t a c a c	t g c t t c t c c c	a t g c c a g a g a	a t a a a c t c t t	t c a a g c a t c a	2707
t c t t t g a a g a	g t c g t g t g g t	g t g a a t t g g t	t t g t g t a c a t	t a g a a t g t a t	g c a c a c a t c c	2767
a t g g a c a c t c	a g g a t a t a g t	t g g c c t a a t a	a t c g g g g c a t	g g g t a a a a c t	t a t g a a a a t t	2827
t c c t c a t g c t	g a a t t g t a a t	t t t c t c t t a c	c t g t a a a g t a	a a a t t t a g a t	c a a t t c c a t g	2887
t c t t t g t t a a	g t a c a g g g a t	t t a a t a t a t t	t t g a a t a t a a	t g g g t a t g t t	c t a a a t t t g a	2947
a c t t t g a g a g	g c a a t a c t g t	t g g a a t t a t g	t g g a t t c t a a	c t c a t t t t a a	c a a g g t a g c c	3007
t g a c t g c a t	a a g a t c a c t t	g a a t g t t a g g	t t c t a t a g a a	c t a t a c t a a t	c t t c t c a c a a	3067
a a g g t c t a t a	a a a t a c a g t c	g t t g a a a a a a	a t t t t g t a t c	a a a a t g t t t g	g a a a a t t a g a	3127
a g c t t c t c c t	t a a c c t g t a t	t g a t a c t g a c	t t g a a t t a t t	t t c t a a a a t t	a a g a g c c g t a	3187
t a c c t a c c t g	t a a g t c t t t t	c a c a t a t c a t	t t a a a c t t t t	g t t t g t a t t a	t t a c t g a t t t	3247
a c a g c t t a g t	t a t t a a t t t t	t c t t t a t a a g	a a t g c c g t c g	a t g t g c a t g c	t t t t a t g t t t	3307
t t c a g a a a a g	g g t g t g t t t g	g a t g a a a g t a	a a a a a a a a a a	t a a a a t c t t t	c a c t g t c t c t	3367
a a t g g c t g t g	c t g t t t a a c a	t t t t t t g a c c	c t a a a a t t c a	c c a a c a g t c t	c c c a g t a c a t	3427
a a a a t a g g c t	t a a t g a c t g g	c c c t g c a t t c	t t c a c a a t a t	t t t t c c c t a a	g c t t t g a g c a	3487
a a g t t t t a a a	a a a a t a c a c t	a a a a t a a t c a	a a a c t g t t a a	g c a g t a t a t t	a g t t t g g t t a	3547
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t a a a a g t g c c	g a t c t g g c t a	a c t c t t a c a c	c a t a c a t a c t	g a t a g t t t t t	c a t a t g t t t c	3727
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a g c t t t a t t t	t t t c c t t t g t	t c a t a a t t a t	a t t c t t t g a a	t a g g t c t g t g	t c a a t c a a g t	3847
g a t c a t a a c t a	a g a t g a t c a t	a g a t a g a a g g	a a a t a a a g c c	a a g t t c a a g a	c c a g c c t g g g	3907
c a c a t a t c g	a g a a c c t g t c	t a c a a a a a a a	t t a a a a a a a a	t t a g c c a g g c	a t g g t g g c g t	3967
a c a c t g a g t a	g t t t g t c c c a	g c t a c t c g g g	a g g g t g a g g t	g g g a g g a t c g	c t t c a g c c c a	4027
g g a g g t t g a g	a t t g c a g t g a	g c c a t g g a c a	t a c c a c t g c a	c t a c a g c c t a	g g t a a c a g c a	4087
c g a g a c c c c a	a c t c t t a g a a	a a t g a a a a g g	a a a t a t a g a a	a t a t a a a a t t	t g c t t a t t a t	4147
a g a c a c a c a g	t a a c t c c c a g	a t a t g t a c c a	c a a a a a a t g t	g a a a a g a g a g	a g a a a t g t c t	4207
a c c a a a g c a g	t a t t t t g t g t	g t a t a a t t g c	a a g c g c a t a g	t a a a a t a a t t	t t a a c c t t a a	4267
t t t g t t t t t a	g t a g t g t t t a	g a t t g a a g a t	t g a g t g a a a t	a t t t t c t t g g	c a g a t a t t c c	4327
g t a t c t g g t g	g a a a g c t a c a	a t g c a a t g t c	g t t g t a g t t t	t g c a t g g c t t	g c t t t a t a a a	4387
c a a g a t t t t t	t c t c c c t c c t	t t t g g g c c a g	t t t t c a t t a c	g a g t a a c t c a	c a c t t t t t g a	4447
t t a a a g a a c t	t g a a a t t a c g	t t a t c a c t t a	g t a t a a t t g a	c a t t a t a t a g	a g a c t a t g t a	4507
a c a t g c a a t c	a t t a g a a t c a	a a a t t a g t a c	t t t g g t c a a a	a t a t t t a c a a	c a t t c a c a t a	4567
c t t g t c a a a t	a t t c a t g t a a	t t a a c t g a a t	t t a a a a c c t t	c a a c t a t t a t	g a a g t g c t c g	4627

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

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ctgaagtact tctaataatac tgaggggaagt ataatatgtg gaacaaaactc tcaacaaaat 4927
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&lt;210&gt; 70

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

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Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
          35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
          50          55          60
Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
65          70          75          80
Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
          85          90          95
Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
          100         105         110
Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
          115         120         125
Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
          130         135         140
Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe
145         150         155         160
Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala
          165         170         175
Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val Leu Lys His Val
          180         185         190
Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys Met Lys
          195         200         205
Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu Gly Lys
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225

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&lt;213&gt; Homo sapiens

&lt;400&gt; 71

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Trp Thr Leu Trp Arg Val Leu Ser Ala Leu Met Pro Ala Arg Leu Tyr
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Gln Arg Val Asp Asp Arg Leu Tyr Cys Val Tyr Gln Asn Met Val Leu
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Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
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Gln Arg Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg Ile Lys
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Ala Thr His Val Ala Phe Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile
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Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys Asp
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Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg Arg Lys
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Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys Thr
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Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu Met
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Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr Gly Thr

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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
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gac cgg ctg tac tgc gtc tac cag agc atg gtg ctc ttc ttc ttc gag 198
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&lt;223&gt; AATAAA

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Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
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Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
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Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
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Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu Gly His Val
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Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe
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Tyr Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val			
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Thr Ile Lys Ala *			
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<210> 124
<211> 5324
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
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<221> polyA_signal
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[illegible]



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&lt;210&gt; 125

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1           5           10          15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Leu Thr
50          55          60
Gly Leu Leu Leu Thr Ser Trp Pro Ser Gly Arg Met Arg

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<211> 238  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> 98...103  
 <223> Box II

<400> 126  
 Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr  
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 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro  
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 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln  
 35 40 45  
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln His Gly  
 50 55 60  
 Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg  
 65 70 75 80  
 Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val  
 85 90 95  
 Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu  
 100 105 110  
 Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Glu Phe Leu Cys Lys Glu  
 115 120 125  
 Cys Pro Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val  
 130 135 140  
 Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu  
 145 150 155 160  
 Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu  
 165 170 175  
 Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile  
 180 185 190  
 Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly  
 195 200 205  
 Met Leu Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile  
 210 215 220  
 Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala  
 225 230 235

<210> 127  
 <211> 291  
 <212> PFT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> 98...103  
 <223> Box II

<221> SITE  
 <222> 149...157

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1           5           10           15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
      20           25           30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
      35           40           45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln His Gly
      50           55           60
Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg
      65           70           75           80
Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val
      85           90           95
Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu
      100          105          110
Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val Leu Lys
      115          120          125
His Val Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys
      130          135          140
Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu
      145          150          155          160
Gly Lys Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met Thr Glu
      165          170          175
Phe Leu Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp Arg Ile
      180          185          190
Asp Lys Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu
      195          200          205
His Glu Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu
      210          215          220
Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn
      225          230          235          240
Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser
      245          250          255
Gly Leu Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys Leu Tyr
      260          265          270
Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val Thr
      275          280          285
Ile Lys Ala
      290

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&lt;210&gt; 128

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; 68..73

&lt;223&gt; Box II

&lt;221&gt; SITE

&lt;222&gt; 119..127

&lt;223&gt; Box III

&lt;400&gt; 128

Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln  
 35 40 45  
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Met Tyr  
 50 55 60  
 Leu Val Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys  
 65 70 75 80  
 Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val  
 85 90 95  
 Leu Lys His Val Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe  
 100 105 110  
 Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val  
 115 120 125  
 Tyr Glu Gly Lys Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met  
 130 135 140  
 Thr Glu Phe Leu Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp  
 145 150 155 160  
 Arg Ile Asp Lys Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg  
 165 170 175  
 Trp Leu His Glu Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe  
 180 185 190  
 Tyr Glu Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser  
 195 200 205  
 Val Asn Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile  
 210 215 220  
 Leu Ser Gly Leu Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys  
 225 230 235 240  
 Leu Tyr Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp  
 245 250 255  
 Val Thr Ile Lys Ala  
 260

&lt;210&gt; 129

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr  
 1 5 10 15  
 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro  
 20 25 30  
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln  
 35 40 45  
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Asn Phe  
 50 55 60  
 Ser Ala Lys Asn Val Gln Lys Phe Ile Phe Thr Leu Ile Val Ser Thr  
 65 70 75 80  
 Lys Lys Met Ser Gln Lys Asn Lys Asn Ile  
 85 90

&lt;210&gt; 130

&lt;211&gt; 68

&lt;212&gt; PRT

Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro  
                   20                  25                  30  
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln  
                   35                  40                  45  
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Asp Ala  
                   50                  55                  60  
 Tyr Arg Ile Leu  
 65

<210> 131  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens  
 <400> 131

Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr  
 1                  5                  10                  15  
 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro  
                   20                  25                  30  
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln  
                   35                  40                  45  
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Arg Leu  
                   50                  55                  60  
 Asp Ser  
 65

<210> 132  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> 81..83  
 <223> Box I

<400> 132  
 Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr  
 1                  5                  10                  15  
 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro  
                   20                  25                  30  
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln  
                   35                  40                  45  
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu  
                   50                  55                  60  
 Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala  
 65                  70                  75                  80  
 Asn His Gln Ser Thr Asp Val Ser Cys Asp Phe Ser Arg Arg Tyr Lys  
                   85                  90                  95  
 Val

<210> 133

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; 81..83

&lt;223&gt; Box I

&lt;400&gt; 133

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1          5          10          15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
50          55          60
Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
65          70          75          80
Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
85          90          95
Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
100         105         110
Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
115         120         125
Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
130         135         140
Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Asn Phe Ser Ala Lys Asn
145         150         155         160
Val Gln Lys Phe Ile Phe Thr Leu Ile Val Ser Thr Lys Lys Met Ser
165         170         175
Gln Lys Asn Lys Asn Ile
180

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&lt;210&gt; 134

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; 81..83

&lt;223&gt; Box I

&lt;221&gt; SITE

&lt;222&gt; 160..165

&lt;223&gt; Box II

&lt;400&gt; 134

```

Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1          5          10          15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu

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<210> 135
<211> 300
<212> PRT
<213> Homo sapiens
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<220>  
<221> SITE  
<222> 81..83  
<223> Box I  
  
<221> SITE  
<222> 160..165  
<223> Box II
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14005 135															
Met	Arg	Tyr	Leu	Leu	Pro	Ser	Val	Val	Leu	Leu	Gly	Thr	Ala	Pro	Thr
1				5					10					15	
Tyr	Val	Leu	Ala	Trp	Gly	Val	Trp	Arg	Leu	Leu	Ser	Ala	Phe	Leu	Pro
			20					25					30		
Ala	Arg	Phe	Tyr	Gln	Ala	Leu	Asp	Asp	Arg	Leu	Tyr	Cys	Val	Tyr	Gln
		35					40					45			
Ser	Met	Val	Leu	Phe	Phe	Phe	Glu	Asn	Tyr	Thr	Gly	Val	Gln	Ile	Leu
	50					55					60				

```

Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
      100                      105                      110
Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
      115                      120                      125
Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
      130                      135                      140
Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe
      145                      150                      155                      160
Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala
      165                      170                      175
Ser Gln Ala Phe Ala Ala Gln Arg Glu Phe Leu Cys Lys Glu Cys Pro
      180                      185                      190
Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro Glu
      195                      200                      205
Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys
      210                      215                      220
Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg Arg
      225                      230                      235                      240
Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys
      245                      250                      255
Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu
      260                      265                      270
Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr Gly
      275                      280                      285
Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala
      290                      295                      300

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<210> 136  
 <211> 185  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> 81..83  
 <223> Box I

<221> SITE  
 <222> 160..165  
 <223> Box II

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<400> 136
Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
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Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
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Sequence(s) identified: 100% identical to the reference sequence (GEN-T113XC3D2) (NCBI accession: F01133.1)

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<221> primer\_bind

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<221> primer\_bind  
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<400> 273

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<221> allele  
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<221> primer\_bind  
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<400> 274  
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<221> allele  
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<223> base T ; A in SEQ ID198

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<221> primer\_bind  
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<400> 275  
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<210> 276  
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<222> 1..47  
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<221> allele  
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<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 4-4-288.mis1

<221> primer\_bind  
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<400> 276  
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<210> 277  
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<221> allele  
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<223> base T ; C in SEQ ID200

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<221> primer\_bind  
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<400> 277  
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<210> 278  
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<221> primer\_bind  
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<400> 278  
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<221> allele  
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<221> primer\_bind  
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<400> 279  
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<221> allele  
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<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-43-70.mis2

<400> 280

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<210> 281

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<221> allele

<222> 24

<223> base T ; C in SEQ ID204

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 4-50-209.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-50-209.mis2

<400> 281

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<210> 282

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<221> allele

<222> 24

<223> base T ; G in SEQ ID205

<221> primer\_bind

<222> 1..23

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<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-50-293.mis2

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<221> allele  
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<400> 283  
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<210> 284  
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<221> allele  
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<223> base T ; C in SEQ ID207

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<222> 1..23  
<223> potential microsequencing oligo 4 50 329.mis1

<221> primer\_bind  
<222> 25..47  
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<400> 284  
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<210> 285

<220>  
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<221> allele  
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<223> base T ; A in SEQ ID208

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<223> potential microsequencing oligo 4-50-330.mis1

<221> primer\_bind  
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<400> 285  
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<210> 286  
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<221> allele  
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<223> potential microsequencing oligo 4-52-163.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 4-52-163.mis2

<400> 286  
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<210> 287  
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<400> 287  
tccatgtcat tattattcaa aagtttaaaa aatacacaag gtgaaaa 47

<210> 288  
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<221> primer\_bind  
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<400> 288  
gagaaatcat gcagagagaa tgcgttctca ctcaaatttt aacctaa 47

<210> 289  
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<223> base T ; A in SEQ ID212

<221> primer\_bind  
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<400> 289  
aagtagtttt tcacactttc tctttgatac aatcgatggc ttaatct

47

<210> 290  
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<221> allele  
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<221> primer\_bind  
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<223> potential microsequencing oligo 4-54-388.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 4-54-388.mis2

<400> 290  
ctctctatcg tatacatctt tacccacgct gcagcgccaa gactcca

47

<210> 291  
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<221> allele  
<222> 24  
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<221> primer\_bind  
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<221> primer\_bind  
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tattaagaac ctaggtttta aaatactctc tatcgtatac atctttta

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<210> 292  
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<223> polymorphic fragment 4-55-95, variant version of SEQ ID215

<221> allele  
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<223> base C ; A in SEQ ID215

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<223> potential microsequencing oligo 4-55-95.mis1

<221> primer\_bind  
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<400> 292  
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<210> 293  
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<221> allele  
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<223> potential microsequencing oligo 4-56-159.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 4-56-159.mis2

<400> 293  
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<213> Homo Sapiens

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<222> 1..47

<223> polymorphic fragment 4-56-213, variant version of SEQ ID217

<221> allele

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<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 4-56-213.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-56-213.mis2

<400> 294

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<210> 295

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

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<222> 1..47

<223> polymorphic fragment 4-58-289, variant version of SEQ ID218

<221> allele

<222> 24

<223> base C ; G in SEQ ID218

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 4-58-289.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 4 58 289.mis2

<400> 295

ataacttgca gcttgctttt ggtcaggggt gactacttta cctgcaa

47

<210> 296

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele  
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<223> base C ; A in SEQ ID219

<221> primer\_bind  
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<223> potential microsequencing oligo 4-58-318.mis1

<221> primer\_bind  
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<400> 296  
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<210> 297  
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<221> allele  
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<223> base T ; G in SEQ ID220

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<222> 1..23  
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<221> primer\_bind  
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aacaggacca agacactgca ttatataaag tttcagtatt tcttagc

47

<210> 298  
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<222> 1..23  
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<221> primer\_bind  
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<223> complement potential microsequencing oligo 4-60-293.mis2

<400> 298  
aagtttcagt atttcttagc agatgaagcc agcaggaagt cctccta

47

<210> 299  
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<221> allele  
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<223> potential microsequencing oligo 4-84-241.mis1

<221> primer\_bind  
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<210> 300  
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<221> allele  
<222> 24  
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<221> allele  
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<221> primer\_bind  
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<210> 302  
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<221> allele  
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<221> primer\_bind  
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<400> 302

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<221> allele  
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<221> primer\_bind  
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<223> potential microsequencing oligo 4-88-349.mis1

<221> primer\_bind  
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<400> 303  
gaaactaaaa gacaatatcc agtctgagat tttccaagtt ctttatg

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<210> 304  
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<221> allele  
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<223> potential microsequencing oligo 4-89-87.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 4 89 87.mis2

<400> 304  
ttcttcctg aacgctgggt tcatatagtt tttgtgtga gaataga

47

<210> 305  
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<221> allele  
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<221> primer\_bind  
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<223> potential microsequencing oligo 99-123-184.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-123-184.mis2

<400> 305  
ccagcccaga acattcacca gctcggccaa gagttctgct gggtttt

47

<210> 306  
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<220>  
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<223> polymorphic fragment 99-128-202, variant version of SEQ ID229

<221> allele  
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<223> base C ; A in SEQ ID229

<221> primer\_bind  
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<223> potential microsequencing oligo 99-128-202.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-128-202.mis2

<400> 306  
aatgtctggt tcttagagaa ctgcaacaca cacacatata tacacac

47

<210> 307  
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<220>  
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<222> 1..47  
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<221> primer\_bind  
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<223> potential microsequencing oligo 99-128-275.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-128-275.mis2

<400> 307  
acaccctac ctcacatgtg taggcaaag tatgcatata tgtctct

47

<210> 308  
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<223> polymorphic fragment 99-128-313, variant version of SEQ ID231

<221> allele  
<222> 24  
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<222> 1..23  
<223> potential microsequencing oligo 99-128-313.mis1

<221> primer\_bind  
<222> 25..47  
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<400> 308  
tatgtctcta gacagatata catgagattc tatttggcat agaaaaa

47

<210> 309  
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<220>  
<221> allele  
<222> 1..47  
<223> polymorphic fragment 99-128-60, variant version of SEQ ID232

<221> allele  
<222> 24  
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<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-128-60.mis2

<400> 309

gcactgtgac ccaggcgcta gggtcctctt acagtgcac tccgaca

47

<210> 310

<211> 47

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<222> 1..47

<223> polymorphic fragment 99-12907-295, variant version of SEQ ID233

<221> allele

<222> 24

<223> base G ; A in SEQ ID233

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 99-12907-295.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-12907-295.mis2

<400> 310

gctatatggc attatatctc cacggggcag acctgatgta caagatg

47

<210> 311

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<223> polymorphic fragment 99-130-58, variant version of SEQ ID234

<221> allele

<222> 24

<223> base T ; C in SEQ ID234

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 99-130-58.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-130-58.mis2

<210> 312  
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<223> polymorphic fragment 99-134-362, variant version of SEQ ID235

<221> allele  
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<223> base T ; G in SEQ ID235

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-134-362.mis1

<221> primer\_bind  
<222> 25..47  
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<400> 312  
caaaacactc atgtagtta gattattatt cctattacaa agataag

47

<210> 313  
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<212> DNA  
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<220>  
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<222> 1..47  
<223> polymorphic fragment 99-140-130, variant version of SEQ ID236

<221> allele  
<222> 24  
<223> base T ; C in SEQ ID236

<221> primer\_bind  
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<221> primer\_bind  
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<400> 313  
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<210> 314

<220>  
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<222> 1..47  
<223> polymorphic fragment 99-1462-238, variant version of SEQ ID237

<221> allele  
<222> 24  
<223> base C ; G in SEQ ID237

<221> primer\_bind  
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<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-1462-238.mis2

<400> 314  
ccctttcaag gttagtaact catctgctgt gtttctgctt cagaagg

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<210> 315  
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<221> allele  
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<223> base G ; A in SEQ ID238

<221> primer\_bind  
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<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-147-181.mis2

<400> 315  
gtgtcatgaa aaagagcatg atagaaagaa aaacttaaat ctttata

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<222> 24  
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<222> 1..23  
<223> potential microsequencing oligo 99-1474-156.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-1474-156.mis2

<400> 316  
cttgactca taagttaaatt attataaca agaagaaata tggactt 47

<210> 317  
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<221> allele  
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<223> base G ; A in SEQ ID240

<221> primer\_bind  
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<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-1474-359.mis2

<400> 317  
aaaaaaaaatc aaattattgt accgaattcc ctaatatcag atgtgta 47

<210> 318  
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<223> polymorphic fragment 99-1479-158, variant version of SEQ ID241

<221> allele  
<222> 24  
<223> base T ; C in SEQ ID241

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-1479-158.mis2

<400> 318  
tttaaaaatc cacttgtaat cgctgctaattggagtgtat attcagg 47

<210> 319  
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<223> polymorphic fragment 99-1479-379, variant version of SEQ ID242

<221> allele  
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<223> base G ; A in SEQ ID242

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-1479-379.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-1479-379.mis2

<400> 319  
gtagagctgt gtactgaggt caggaagca gctcatggta cagcctt 47

<210> 320  
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<221> allele  
<222> 24  
<223> base G ; A in SEQ ID243

<221> primer\_bind  
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<221> primer\_bind

ttcatatcta tacaaataat tttgaattta atacataggg ctgcaaaa

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<210> 321  
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<223> polymorphic fragment 99-148-132, variant version of SEQ ID244

<221> allele  
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<223> base T ; C in SEQ ID244

<221> primer\_bind  
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<223> potential microsequencing oligo 99-148-132.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-148-132.mis2

<400> 321  
atatctatac aaataatttt gaatttaata catagggctg caaaaca

47

<210> 322  
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<212> DNA  
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<220>  
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<222> 1..47  
<223> polymorphic fragment 99-148-139, variant version of SEQ ID245

<221> allele  
<222> 24  
<223> base T ; C in SEQ ID245

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-148-139.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-148-139.mis2

<400> 322  
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<213> Homo Sapiens

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<221> allele

<222> 1..47

<223> polymorphic fragment 99-148-140, variant version of SEQ ID246

<221> allele

<222> 24

<223> base G ; A in SEQ ID246

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 99-148-140.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-148-140.mis2

<400> 323

acaaataatt ttgaatttaa tacgtagggc tgcaaaacaa ggttgat

47

<210> 324

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-148-182, variant version of SEQ ID247

<221> allele

<222> 24

<223> base G ; A in SEQ ID247

<221> primer\_bind

<222> 1..23

<223> potential microsequencing oligo 99-148-182.mis1

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-148-182.mis2

<400> 324

ttgatgttga tatgggcaac tgtgtgttgg atggtcccaa agcattc

47

<210> 325

<211> 47

<212> DNA

<213> Homo Sapiens

<221> allele  
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<223> base T ; G in SEQ ID248

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-148-366.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-148-366.mis2

<400> 325  
tccttgtaa aggtctctcc ctgttgctca cggctgccgc ctcaaag

47

<210> 326  
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<220>  
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<221> allele  
<222> 24  
<223> base T ; C in SEQ ID249

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-148-76.mis1

<221> primer\_bind  
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<223> complement potential microsequencing oligo 99-148-76.mis2

<400> 326  
tgatagaatg ccttcctgaa ttattactct tgatggcttc ataaaaac

47

<210> 327  
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<220>  
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<222> 1..47  
<223> polymorphic fragment 99-1480-290, variant version of SEQ ID250

<221> allele

<222> 1..23  
<223> potential microsequencing oligo 99-1480-290.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-1480-290.mis2

<400> 327  
tgcaccatct tcaccacaac ccctggcaac cactgacct tttactg 47

<210> 328  
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<222> 1..47  
<223> polymorphic fragment 99-1481-285, variant version of SEQ ID251

<221> allele  
<222> 24  
<223> base T ; G in SEQ ID251

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-1481-285.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-1481-285.mis2

<400> 328  
tcccataacc tgttttgctt ctctctctaa cctcaagatg gtataaa 47

<210> 329  
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<220>  
<221> allele  
<222> 1..47  
<223> polymorphic fragment 99-1484-101, variant version of SEQ ID252

<221> allele  
<222> 24  
<223> base C ; A in SEQ ID252

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-1484-101.mis1

&lt;400&gt; 329

aaaaagatca aatataagca tgtcactcct ctccttaaaa tctcagt

47

&lt;210&gt; 330

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1..47

&lt;223&gt; polymorphic fragment 99-1484-328, variant version of SEQ ID253

&lt;221&gt; allele

&lt;222&gt; 24

&lt;223&gt; base C ; G in SEQ ID253

&lt;221&gt; primer\_bind

&lt;222&gt; 1..23

&lt;223&gt; potential microsequencing oligo 99-1484-328.mis1

&lt;221&gt; primer\_bind

&lt;222&gt; 25..47

&lt;223&gt; complement potential microsequencing oligo 99-1484-328.mis2

&lt;400&gt; 330

ggacacgtgg tcatgaggag tttcaaggga ttcagttttc agatccc

47

&lt;210&gt; 331

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1..47

&lt;223&gt; polymorphic fragment 99-1485-251, variant version of SEQ ID254

&lt;221&gt; allele

&lt;222&gt; 24

&lt;223&gt; base T ; G in SEQ ID254

&lt;221&gt; primer\_bind

&lt;222&gt; 1..23

&lt;223&gt; potential microsequencing oligo 99-1485-251.mis1

&lt;221&gt; primer\_bind

&lt;222&gt; 25..47

&lt;223&gt; complement potential microsequencing oligo 99-1485-251.mis2

&lt;400&gt; 331

<211> 47  
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<221> allele  
<222> 1..47  
<223> polymorphic fragment 99-1490-381, variant version of SEQ ID255

<221> allele  
<222> 24  
<223> base T ; C in SEQ ID255

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-1490-381.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-1490-381.mis2

<400> 332  
tgcacagtgg aaataccatg tcatggtacg ctactgtgca tctcttc

47

<210> 333  
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<213> Homo Sapiens

<220>  
<221> allele  
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<223> polymorphic fragment 99-1493-280, variant version of SEQ ID256

<221> allele  
<222> 24  
<223> base G ; A in SEQ ID256

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-1493-280.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-1493-280.mis2

<400> 333  
ggatgacaga gtattgttgg agggatgggg tttggctgct tgttttt

47

<210> 334  
<211> 47  
<212> DNA

<222> 1..47  
<223> polymorphic fragment 99-151-94, variant version of SEQ ID257

<221> allele  
<222> 24  
<223> base G ; A in SEQ ID257

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-151-94.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-151-94.mis2

<400> 334  
attgagatca ttgataagga aatgttctaa aatttcacaaa tctatat

47

<210> 335  
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<223> polymorphic fragment 99-211-291, variant version of SEQ ID258

<221> allele  
<222> 24  
<223> base G ; A in SEQ ID258

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-211-291.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-211-291.mis2

<400> 335  
ctgggttatat cagactgacc ttctgtgtttt caacagggtca atgcctt

47

<210> 336  
<211> 46  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 1..46  
<223> polymorphic fragment 99-213-137, variant version of SEQ ID259

<221> primer\_bind  
<222> 1..22  
<223> potential microsequencing oligo 99-213-37.mis1

<221> primer\_bind  
<222> 24..46  
<223> complement potential microsequencing oligo 99-213-37.mis2

<400> 336  
gtgcttcgg ctgcaggact gtgcggagga ctccagtgtc tgacag 46

<210> 337  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
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<222> 1..47  
<223> polymorphic fragment 99-221-442, variant version of SEQ ID260

<221> allele  
<222> 24  
<223> base C ; A in SEQ ID260

<221> primer\_bind  
<222> 1..23  
<223> potential microsequencing oligo 99-221-442.mis1

<221> primer\_bind  
<222> 25..47  
<223> complement potential microsequencing oligo 99-221-442.mis2

<400> 337  
tgcctttgta gatatgcatg ggacttccat gacctagcca gacgaat 47

<210> 338  
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<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 1..47  
<223> polymorphic fragment 99-222-109, variant version of SEQ ID261

<221> allele  
<222> 24  
<223> base T ; C in SEQ ID261

<221> primer\_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-222-109.mis2

<400> 338

caggtgagga gtgctggatt ggctacgata tgaatttctt cagcagt

47

<210> 339

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..18

<223> upstream amplification primer for SEQ 185, SEQ 262, SEQ 186, SEQ 263, SEQ 187, SEQ 264

<400> 339

tctaacctct catccaac

18

<210> 340

<211> 19

<212> DNA

<213> Homo Sapiens

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<221> misc\_feature

<222> 1..19

<223> upstream amplification primer for SEQ 188, SEQ 265, SEQ 189, SEQ 266

<400> 340

gttatcgtga gactttttc

19

<210> 341

<211> 18

<212> DNA

<213> Homo Sapiens

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<221> misc\_feature

<222> 1..18

<223> upstream amplification primer for SEQ 190, SEQ 267, SEQ 191, SEQ 268

<400> 341

tgctggtgct gtgataac

18

<210> 342

<211> 18

<212> DNA

<213> Homo Sapiens

<223> upstream amplification primer for SEQ 192, SEQ 269, SEQ 193, SEQ 270

<400> 342

tacagccctg taagacac

18

<210> 343

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..19

<223> upstream amplification primer for SEQ 194, SEQ 271

<400> 343

cagtatgttc aatgcacag

19

<210> 344

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..18

<223> upstream amplification primer for SEQ 195, SEQ 272, SEQ 196, SEQ 273

<400> 344

aaaacatcga catgggac

18

<210> 345

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..18

<223> upstream amplification primer for SEQ 197, SEQ 274, SEQ 198, SEQ 275, SEQ 199, SEQ 276

<400> 345

agcatttcga gtcatgtg

18

<210> 346

<211> 18

<212> DNA

<213> Homo Sapiens

<400> 346  
ccctctttcc tcatgtag 18

<210> 347  
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<220>  
<221> misc\_feature  
<222> 1..19  
<223> upstream amplification primer for SEQ 202, SEQ 279, SEQ 203, SEQ 280

<400> 347  
taactcgtaa acagagaac 19

<210> 348  
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<221> misc\_feature  
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<223> upstream amplification primer for SEQ 204, SEQ 281, SEQ 205, SEQ 282, SEQ 206, SEQ 283, SEQ 207, SEQ 284, SEQ 208, SEQ 285

<400> 348  
gcgtattgaa gctctttg 18

<210> 349  
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<220>  
<221> misc\_feature  
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<223> upstream amplification primer for SEQ 209, SEQ 286, SEQ 210, SEQ 287

<400> 349  
aacacgggga ttttaggc 18

<210> 350  
<211> 19  
<212> DNA  
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<220>

<400> 350  
cacatactaa ggctaattg

19

<210> 351  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 212, SEQ 289, SEQ 213, SEQ 290

<400> 351  
gttgctggaa cctatttg

18

<210> 352  
<211> 18  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 214, SEQ 291, SEQ 215, SEQ 292

<400> 352  
tcgatggctt aatctacc

18

<210> 353  
<211> 18  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 216, SEQ 293, SEQ 217, SEQ 294

<400> 353  
aaagaggagt aaatgggg

18

<210> 354  
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<212> DNA  
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<220>  
<221> misc\_feature  
<222> 1..18

<210> 355  
<211> 18  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 220, SEQ 297, SEQ 221, SEQ 298

<400> 355  
atacctaatt tcaggggg 18

<210> 356  
<211> 19  
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<223> upstream amplification primer for SEQ 222, SEQ 299, SEQ 223, SEQ 300

<400> 356  
ttaacagagt accttgag 19

<210> 357  
<211> 18  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 224, SEQ 301, SEQ 225, SEQ 302

<400> 357  
gtacagcctt ttgcttac 18

<210> 358  
<211> 18  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 226, SEQ 303

<210> 359  
<211> 19  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> misc\_feature  
<222> 1..19  
<223> upstream amplification primer for SEQ 227, SEQ 304

<400> 359  
gctgatgagt tagataacc 19

<210> 360  
<211> 18  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 228, SEQ 305

<400> 360  
aaagccagga ctagaagg 18

<210> 361  
<211> 18  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 229, SEQ 306, SEQ 230, SEQ 307,  
SEQ 231, SEQ 308, SEQ 232, SEQ 309

<400> 361  
gaccagggtt taagttag 18

<210> 362  
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<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 233, SEQ 310

<400> 362

<211> 19  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> 1..19  
<223> upstream amplification primer for SEQ 234, SEQ 311

<400> 363  
ccataacagc tagtacaac 19

<210> 364  
<211> 18  
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<220>  
<221> misc\_feature  
<222> 1..18  
<223> upstream amplification primer for SEQ 235, SEQ 312

<400> 364  
tggaaggta ctcagaag 18

<210> 365  
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<220>  
<221> misc\_feature  
<222> 1..19  
<223> upstream amplification primer for SEQ 236, SEQ 313

<400> 365  
agagcatagt ataaagcag 19

<210> 366  
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<221> misc\_feature  
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<223> upstream amplification primer for SEQ 237, SEQ 314

<400> 366  
ctagaagtag cttaacag 19

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..19

<223> upstream amplification primer for SEQ 238, SEQ 315

<400> 367

gcagccaatc ttatatattc

19

<210> 368

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..19

<223> upstream amplification primer for SEQ 239, SEQ 316, SEQ 240, SEQ 317

<400> 368

aaggttgtag agtagaaag

19

<210> 369

<211> 18

<212> DNA

<213> Homo Sapiens

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<221> misc\_feature

<222> 1..18

<223> upstream amplification primer for SEQ 241, SEQ 318, SEQ 242, SEQ 319

<400> 369

caactgacac tataaccc

18

<210> 370

<211> 18

<212> DNA

<213> Homo Sapiens

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<221> misc\_feature

<222> 1..18

<223> upstream amplification primer for SEQ 243, SEQ 320, SEQ 244, SEQ 321, SEQ 245, SEQ 322, SEQ 246, SEQ 323, SEQ 247, SEQ 324, SEQ 248, SEQ 325, SEQ 249, SEQ 326

<400> 370

cagtggagtg tttatgtg

18

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..19

<223> upstream amplification primer for SEQ 250, SEQ 327

<400> 371

ttgcacaaaa ggtatagag

19

<210> 372

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..19

<223> upstream amplification primer for SEQ 251, SEQ 328

<400> 372

aggctcccct ttgagttg

19

<210> 373

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..18

<223> upstream amplification primer for SEQ 252, SEQ 329, SEQ 253, SEQ 330

<400> 373

atcctttcta gctgggag

18

<210> 374

<211> 20

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> 1..20

<223> upstream amplification primer for SEQ 254, SEQ 331

<400> 374

gtttaagaat gtgtgatggg

20

<210> 375

<220>  
<221> misc\_feature  
<222> 1..19  
<223> upstream amplification primer for SEQ 255, SEQ 332

<400> 375  
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tccttacttg taaccccc 18

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<223> upstream amplification primer for SEQ 259, SEQ 336

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<210> 380

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<223> upstream amplification primer for SEQ 260, SEQ 337

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<210> 381

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<223> upstream amplification primer for SEQ 261, SEQ 338

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<223> downstream amplification primer for SEQ 185, SEQ 262, SEQ 186, SEQ 263, SEQ 187, SEQ 264

<400> 382

gactgtatcc tttgatgcac

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<210> 383

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<223> downstream amplification primer for SEQ 188, SEQ 265, SEQ 189, SEQ 266

<400> 383

gcataattgt gcttgactgg

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<210> 384

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<223> downstream amplification primer for SEQ 190, SEQ 267, SEQ 191, SEQ 268

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18

<210> 385

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18

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<400> 387  
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SEQ 199, SEQ 276

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<400> 391  
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tataagcaca aatagggtcc 20

<210> 394  
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ctaaggtgtt gtagacag 18

<210> 397  
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cacctcgata aatcaagtcc 20

<210> 398  
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<210> 399  
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<400> 402  
agcaagagtg attgtaaag 19

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<223> downstream amplification primer for SEQ 228, SEQ 305

<400> 403  
tattcaqaaa ggaqtggg 18

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SEQ 231, SEQ 308, SEQ 232, SEQ 309  
  
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<400> 406  
agaaaccata aggttatatt g 21  
  
<210> 407  
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acagtgcaaa gggttatatc 19

<213> Homo Sapiens

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<223> downstream amplification primer for SEQ 236, SEQ 313

<400> 408

gaacaacctt gaattagctt g

21

<210> 409

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<222> 1..21

<223> downstream amplification primer for SEQ 237, SEQ 314

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gattccagaa gtccatttca g

21

<210> 410

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<222> 1..21

<223> downstream amplification primer for SEQ 238, SEQ 315

<400> 410

aggtaagaat gagcaaaaag g

21

<210> 411

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<223> downstream amplification primer for SEQ 239, SEQ 316, SEQ 240, SEQ 317

<400> 411

gcttgtgttt gttcaattc

19

<210> 412

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<223> downstream amplification primer for SEQ 241, SEQ 318, SEQ 242, SEQ 319

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<223> downstream amplification primer for SEQ 252, SEQ 329, SEQ 253, SEQ 330

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<223> downstream amplification primer for SEQ 255, SEQ 332

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<400> 419  
ccttttatatc cttggagtc 19

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<223> downstream amplification primer for SEQ 257, SEQ 334

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21

<210> 421

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<223> downstream amplification primer for SEQ 259, SEQ 336

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<210> 423

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<223> downstream amplification primer for SEQ 260, SEQ 337

<400> 423

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<400> 424  
gaaacagact gaagcaagga c

21

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acaaccacca aatgcatac

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<400> 426  
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tttttgctgt gtcttcaaag tga

23

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<400> 435  
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<400> 436

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<400> 438  
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23

<210> 442

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19

<210> 443

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<210> 444

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23

<210> 445

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<400> 445  
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23

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<400> 448  
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19

<210> 449  
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<210> 450  
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23

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aatcatgcag agagaatgc

19

<210> 452  
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<400> 452  
aagtagtttt tcacactttc tct

23

<210> 453  
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<400> 453  
ctatcgtata catctttac

19

<210> 454  
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<400> 454  
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19

<210> 455  
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<400> 455  
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23

<210> 456  
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<400> 456  
aagttttcct tctctttctgt aga

23

<210> 457  
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ctcatgttca ctctggttc

19

<210> 458  
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<400> 458  
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23

<210> 459  
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<400> 459  
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23

<210> 460  
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<400> 460  
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23

<210> 461  
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<210> 462  
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<400> 465

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<400> 466  
ctaaaagaca atattcagt 19

<210> 467  
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